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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,372CDATE: 06/28/2002
TIME: 14:12:02Input Set : A:\61302updated.ST25.txt
Output Set: N:\CRF3\06282002\J017372C.raw

3 <110> APPLICANT: Wolfrain, Lawrence A
4 Letterio, John J
6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
8 <130> FILE REFERENCE: 4239-61302
10 <140> CURRENT APPLICATION NUMBER: US 10/017,372C
11 <141> CURRENT FILING DATE: 2001-10-19
13 <150> PRIOR APPLICATION NUMBER: US 60/242,292
14 <151> PRIOR FILING DATE: 2000-10-20
16 <160> NUMBER OF SEQ ID NOS: 39
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 28
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Primer
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35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Primer
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47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
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57 <211> LENGTH: 45
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Primer
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65 cttgtcgtcg tcatccttgt agtctcgccg gtgccggag ctgtg
68 <210> SEQ ID NO: 5

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69 <211> LENGTH: 45
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Artificial Sequence
 73 <220> FEATURE:
 74 <223> OTHER INFORMATION: Primer
 76 <400> SEQUENCE: 5
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 81 <211> LENGTH: 45
 82 <212> TYPE: DNA
 83 <213> ORGANISM: Artificial Sequence
 85 <220> FEATURE:
 86 <223> OTHER INFORMATION: Primer
 88 <400> SEQUENCE: 6
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 93 <211> LENGTH: 8
 94 <212> TYPE: PRT
 95 <213> ORGANISM: Artificial Sequence
 97 <220> FEATURE:
 98 <223> OTHER INFORMATION: Synthetic oligopeptide
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 103 1 5
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 107 <211> LENGTH: 1197
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 109 <213> ORGANISM: Artificial Sequence
 111 <220> FEATURE:
 112 <223> OTHER INFORMATION: Fusion oligonucleotide
 114 <220> FEATURE:
 115 <221> NAME/KEY: CDS
 116 <222> LOCATION: (1)..(1197)
 117 <223> OTHER INFORMATION:
 120 <220> FEATURE:
 121 <221> NAME/KEY: misc_feature
 122 <222> LOCATION: (278)..(279)
 123 <223> OTHER INFORMATION: Maturation cleavage site
 126 <400> SEQUENCE: 8
 127 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ctg 48
 128 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Leu
 129 1 5 10 15
 131 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gca ctg tcc acc 96
 132 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 133 20 25 30
 135 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
 136 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 137 35 40 45
 139 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccc agc 192

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140	Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser			
141	50	55	60	
143	cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt	240		
144	Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu			
145	65	70	75	80
147	tac aac agt acc cgc gac cggt gta gcc ggg gaa agt gtc gaa ccg gag	288		
148	Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu			
149	85	90	95	
151	ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta	336		
152	Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu			
153	100	105	110	
155	atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc	384		
156	Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro			
157	115	120	125	
159	cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg	432		
160	His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val			
161	130	135	140	
163	ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc	480		
164	Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Arg Leu			
165	145	150	155	160
167	aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat	528		
168	Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn			
169	165	170	175	
171	gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca	576		
172	Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser			
173	180	185	190	
175	ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg	624		
176	Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu			
177	195	200	205	
179	acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc	672		
180	Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser			
181	210	215	220	
183	tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat	720		
184	Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn			
185	225	230	235	240
187	tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc	768		
188	Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro			
189	245	250	255	
191	tcc ctg ctc atg gcc acc cgg ctg gag agg gcc cag cac ctg cac	816		
192	Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His			
193	260	265	270	
195	agc tcc cgg cac cgc cga gac tac aag gat gac gac aag gcc ctg	864		
196	Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Lys Ala Leu			
197	275	280	285	
199	gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg	912		
200	Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg			
201	290	295	300	
203	cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat	960		
204	Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His			

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205	305	310	315	320	
207	gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac				1008
208	Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr				
209	325	330	335		
211	atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac				1056
212	Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn				
213	340	345	350		
215	cag cac aac ccg ggc gcg tcg gcg ccg tgc tgc gtg ccg cag gcg				1104
216	Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala				
217	355	360	365		
219	ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg				1152
220	Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val				
221	370	375	380		
223	gag cag ctg tcc aac atc gtg cgt tcc tgc aag tgc agc tga				1197
224	Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser				
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229	<211> LENGTH: 398				
230	<212> TYPE: PRT				
231	<213> ORGANISM: Artificial Sequence				
233	<220> FEATURE:				
234	<223> OTHER INFORMATION: Fusion oligonucleotide				
236	<220> FEATURE:				
237	<221> NAME/KEY: misc_feature				
238	<222> LOCATION: (278)..(279)				
239	<223> OTHER INFORMATION: Maturation cleavage site				
241	<400> SEQUENCE: 9				
243	Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Leu				
244	1	5	10	15	
247	Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr				
248	20	25	30		
251	Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala				
252	35	40	45		
255	Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser				
256	50	55	60		
259	Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu				
260	65	70	75	80	
263	Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu				
264	85	90	95		
267	Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu				
268	100	105	110		
271	Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro				
272	115	120	125		
275	His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val				
276	130	135	140		
279	Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu				
280	145	150	155	160	
283	Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn				
284	165	170	175		

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287 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
288 180 185 190
291 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
292 195 200 205
295 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
296 210 215 220
299 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
300 225 230 235 240
303 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
304 245 250 255
307 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
308 260 265 270
311 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
312 275 280 285
315 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
316 290 295 300
319 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
320 305 310 315 320
323 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
324 325 330 335
327 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
328 340 345 350
331 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
332 355 360 365
335 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
336 370 375 380
339 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
340 385 390 395
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345 <212> TYPE: DNA
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348 <220> FEATURE:
349 <223> OTHER INFORMATION: Fusion oligonucleotide
351 <400> SEQUENCE: 10
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354 aagaactgct gcgtcgccca gctctacatt gacttccgga aggacctggg ctggaaagtgg 120
356 attcatgaac ccaagggcctc catgccaatt tctgcctggg gccctgtccc tacatctgga 180
358 gccttagacac tcagtagacgc aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt 240
360 cggcggcgcgc gtgctgcgtg ccgcaggcgc tggagccact gccccatcgtg tactacgtgg 300
362 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttccctgc aagtgcagct 360
364 ga 362
367 <210> SEQ ID NO: 11
368 <211> LENGTH: 120
369 <212> TYPE: PRT
370 <213> ORGANISM: Artificial Sequence
372 <220> FEATURE:
373 <223> OTHER INFORMATION: Fusion oligopeptide
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/017,372C

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